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## ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE RESULT 1
AW531158
LOCUS
DEFINITION COMMENT JOURNAL MEDLINE University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7el: 319 335 8250
Fax: 319 335 9565
Email: msoarcs@blue.weeg.uiowa.edu
Email: msoarcs@blue.weeg.uiowa.edu
Coligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; AW531158

413 bp mRNA linear EST 06-MAR-:
UI-R-BT1-akv-d-05-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone
UI-R-BT1-akv-d-05-0-UI 3', mRNA sequence. Contact: Soares, MB
Program for Rat Gene Discovery and Mapping Genome Res. 6 (9), 791-806 (1996) 97044477 1 (bases 1 to 413)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
gormalization and subtraction: two approaches EST discovery Norway rat. AW531158.1 AW531158 Rattus. GI:7173572 ç facilitate gene EST 06-MAR-2000

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Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resge
                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                           BF563910 437 bp mRNA UI-R-BT1-akv-d-05-0-UI.rl UI-R-BT1 Rattus UI-R-BT1-akv-d-05-0-UI 5', mRNA sequence.
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Seq primer: M13 Forward
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library UI-R-BTI is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.liowa.edu. The subtraction has been previously
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TAG_LIB=UI-R-BT1
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/clone="UI-R-BT1-akv-d-05-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ311551
BQ311551.1
                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                             sequence tags
                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                      Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ311551 674 bp mRNA linear RC2-BN0332-200600-011-dl2 BN0332 Homo sapiens cDNA,
Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is also available through the I.M.A.G.E. Consortium LLNL (info@image.llnl.gov). IMAGE ID- 1800144 The following
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/lab_host="pH108 (Life Technologies)"
/lab_host="pH108 (Life Technologies)"
/lab_host="pH108 (Life Technologies)"
/note="vector: pH73D-Pac (Pharmacia) with a modified
/note="vector: pH73D-Pac (Pharmacia) with a modified
/note="vector: pH73D-Pac (Pharmacia) with a modified
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/db_xref="taxon:10116"
/clone="UI-R-BTI-aky-d-05-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
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High quality sequence stop: 671.
Location/Qualifiers
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                                                                                                                                                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Baurin, W. and Weissenbach, J. Brottler, Brown gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                            2 (bases 1 to 1040)
Roest-Crollius, H., Jaillon, O.,
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1 (bases 1 to 1040)
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                                                                                                             Charaterization and repeat analysis of the compact genome of the
                                                                                                                                  Weissenbach,J
                                                                                                                                                       Bouneau, L., Billault, A., Quetier, F., Saurin, W.,
                                                                                                                                                                                                                      Unpublished
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/clone_lib="BN0332"
/dev_stage="Adult"
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library G from Tetraodon nigroviridis, genomic survey
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                                                                                      Tetraodon nigroviridis
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                   Roest-Crollius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr/Tetraodon.
                                                                This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetraodon nigrovirid genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
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166022 of library G from Tetra
                                                                                                                 Submitted (12-APR-2000)
                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                     Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fi
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A.
                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                   treshwater pufferfish
                                                                                                                                                                                                                                       Weissenbach,J.
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1 (bases 1 to 849)
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/note="Genoscope sequence ID : COAG198DG11SP1~end
PUC-Ori"
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/db_xref="taxon:99883"
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/organism="Tetraodon nigroviridis
                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTGTTACTTGAAAGGATCGAGAATGAMGACATCGGGAGGRAGAMMTTGAAGATCACCG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGCTACTTGAGAAGATAGAACATGATGACATCTGCAATAAAACTTTGAAGATTACAG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTICGGGCTGGCCAGGGAGTGGCACAAAAMMACCAAGATGTCGGCTGMAGGCACCTACT 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 486)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                          Plate: 60 row: N column: 23
Seq primer: ATTTAGGTGACACTATAG.
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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94142 MARC 1BOV Bos taurus cDNA 5',
AW658260
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BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 402 762 4366
Fax: 402 762 4390
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/clone="16602"
/clone="lib="G"
/clone="lib="G"
/note="denoscope sequence I
a 219 c 221 g 216 t
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        /tissue_type="pooled"
/lab_host="PH10B"
/lab_host="PH10B"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
155 c 140 g 101 t 1 others
                                                                                                                             /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                          Location/Qualifiers
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Pred. No. 6e-16;
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CACCGAGACCTCAAGTCCAACAACATTCTGCTGCTGCAGCCCATTGAAGGTGACGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 76 row: M column: 8
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                               and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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181081 MARC 4BOV Bos taurus cDNA 5', mRN
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                                                                                                                                           embryos.
a 169
                                                                                                                                                         /note="Vector: pCMV SPORT6; Site
Library made from pooled tissue
embryos."
                                                                                                                                                                                                    /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                     /clone_lib="MARC 4BOV"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No. 5.3e-15;
                                                                                                                                                                   pCMV SPORT6; Site_1: NotI; Site_2 com pooled tissue from day 20 and
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                                                                            DB 10;
5.5e-15;
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AUTHORS
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                                        694 CACCGAGACCTCAAGTCCAACAACATTCTGCTGCTGCAGCCCATTGAAGGTGACGACATG 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
62 TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                 2 CACCGGGACATCAAGGCAAGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAATGAGTGCTGCGGGCACCTATGCCTGGATGGCTCCTGAGG 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCACAAGACCCTGAAGATCACGGACTTCGGTCTGGCCCGTGAGTGGCACAAAACCACG 428
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MI-P-CP1-nzb-a-19-0-UI.sl MI-P-CP1 Sus scrofa
MI-P-CP1-nzb-a-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Dr. Chris Tuggle, Iowa State University cDNA Library preparation: Dr. M. Bento Soares, University of cDNA Library Arrayed by: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Resea Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \begin{array}{ll} \textbf{Contact: Tuggle CK} \\ \textbf{Molecular Genetics Laboratory, Department of} \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97044477
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cktuggle@iastate.edu
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                                                                                                                                                                                                                                          143
                                                                                                                                                                                                                        /organism="Sus scrofa"
/organism="Sus scrofa"
/organism="Crossbreed"
/db_xref="taxon:9823"
/clone_lib="MI-P-CP1"
/clone_lib="MI-P-CP1"
/lab host="NH10B (Life Technologies)"
/lab host="NH10B (Life Technologies)"
/lab host="NH10B (Life Technologies)"
/lab host="Site_1: Not I; Site_2: EcoRI; The MI-P-CP1
library is normalized library derived from the MI-P-CP1
library is normalized library derived from the MI-P-CP0
library oultimately derived from uterus tissue. For a
detailed description of the library from which this clone
was derived, please visit our web site at
http://pigest.genome.lastate.edu/. The procedure used to
create this library has been previously described (Bonaldo
, Lennon and Soares, Genome Research 6: 791-806, 1996)
TAG_SEQ=None found"

143 a 251 c 246 g 151 t
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                                                                                                                                                51.6%;
69.9%;
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                                                                                                                              0;
                                                                                                                                                  Score 84.6; DB 14
Pred. No. 6.2e-15;
                                                                                                                              Mismatches
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                                                                                                                              Indels
                                                                                                                                                                      Length
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Sus.
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                                                                                                                                                                                                                                    CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGATGACATC 61
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                                                                                 CAAATGAGTGCCGCGGCACCTACGCCTGGATGGCTCCTGAGG
                                                                                                                                                                                TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
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                                                                                                                                                                                                                                                                                 al Similarity
113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genomics@hri.co.jp

HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812,
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito, K., Yamamoto, J., Naki, Y., Sugano, S., Isogai, T.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRI human cDNA project (Ota, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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AU125482 NT2RM4 Homo sapiens
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                          /uore="Vector: pME18SFL3; mRNA from uninduced precursor cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4001663"
                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="teratocarcinoma"
/cell_line="NT2"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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69.3%;
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Nakamura,Y., Nishikawa,T., Nagai,T.,
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DEFINITION

BQ719600 873 bp mRNA linear EST 16-JUL-2002 AGENCOURT\_8234446 Lupski\_sympathetic\_trunk Homo sapiens cDNA clone

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BQ719600
BQ719600.1 GI:21858497
Homo sapiens
                                                                                       5', mRNA sequence.
BQ227232
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Contact: Robert Strausberg, Ph.D.
                                                                   BQ227232.1
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Plate: LLAM13584 row: 1 column:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
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National Institutes of Health, Mammalian
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                                  human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Vector: pCMV-SPORT6 (Life Technologies); Site_1: Not1; Site_1: Sall; cDNA made by Oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6188692"
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/sex="male"
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AGENCOURT_6554238 NIH_MGC_72
5', mRNA sequence.
BM5449822
                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1057)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo of the companies of the constructed by Large primer is size 1.8 kb. Library constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large primer is size 1.8 kb. Tibrary constructed by Large p
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/clone_lib="NIH_MGC_68"
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Pred. No. 2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CACCGGGACATCAAGGCAGGAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATC 61
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Plate: LLAM12257 row
                                                                                                                                                                                                                 cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2383 row: f column: 08
High quality sequence stop: 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENCOURT_7975607 NIH_MGC_113
                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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/note="Organ: skin; Vector: pCWV-SPPRT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo |
Average insert size 2 kb. Library constructed by Lif-
Technologies."
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/db_xref="taxon:9606"
/clone="IMAGE:5548665"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the
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                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6215047"
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BG751808
BG751808.1 GI:14062461
EST.
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Tissue Procurement: ATCC
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http://image.llnl.gov
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                               /organism="Homo sapiens"
//db xref="taxon:9606"
//clone="IMAGE:4874218"
//clone=lib="NIH_MCC_43"
//tissue_type="normal pigmented retinal epithelium"
//tissue_type="normal pigmented retinal epithelium"
//lab_host="DH10B (phage-resistant)"
//note="Organ: eye: Vector: poTB7; Site_1: XhoI; Site_2:
//note="Organ: eye: Vector: poTB7; Site_1: XhoI; Site_2: XhoI; Site_3: XhoI; Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 200 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 863
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70.18;
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Pred. No. 4.7e-13;
D; Mismatches 49;
Score 75.2; DB 12;
Pred. No. 4.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    863 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nRNA linear EST 15-MAY-2001 CDNA clone IMAGE:4874218 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene Collection (MGC)
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                             Length 863;
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Matches 101;

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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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ORGANISM
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VERSION
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                                                                                                                                                      Query Match
Best Local Similarity
Matches 108; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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354 GAACACAAGACCCTAAAGATTACTGACTTCGGCCTCGCCCGAGAGTGGCACAAAACCACC
                                                                      294 CACCGAGACCTGAAGTCCAACAACATTCTGTTGCTGCAGCCCATCGAGGGTGACGACATG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCTACGCCTGGATGGCTCCTGAGG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CCTATGCCTGGATGGCCCCAGAAG 164
                                62 TGCAATAAAACTTTGAAGATTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCACCGACTTTGGCCTGGCCCGAGAGTGGCACAAAACCACACAAATGAGTGCCGCGGGCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 GAAATATTTTGCTACTTGAGAAGATAGAACATGATGACATCTGCAATAAAACTTTTGAAGA
                                                                                              2 CACCGGGACATCAAGGCAGGAAATATTTTTGCTACTTGAGAAGATAGAACATGATGATGATGACATC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen/Robin Humphreys
CDNA Library Preparation: Life Technologies
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information car
info@image.llnl.gov
MCI-INACOAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTACAGATTTTGGGTTGGCGAGGGAATGGCACAGGACCACCAAAATGAGCACAGCAGCAC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 461)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461 bp mRNA linear EST 07-MAY-2002
NISC_ff11e05.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2865512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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BQ266193.1
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                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                   /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:2865512"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Pred. No. 4.1e-12;
0; Mismatches 55;
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                                                                                                                                                                                      Length 461;
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Db
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414 CAGATGAGTGCTGCGGGCACCTACGCTTGGATGGCTCCCGAGG
             122 AAAATGAGCACAGCAGCACCTATGCCTGGATGGCCCCAGAAG
456
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Search completed: December 13, 2002, 23:27:10 Job time: 2181 secs